

MDLA_PENCA	KLQSR-----DVSTSELDQFEFWVQYAAASY-----	47
	. ** . . . . *	
LIP_RHIDL	GGMTLDLPSDAPPISLSSSTNSASDGGKVVAATTAQIQEFTKYAGIAATA	150
LIP_RHIMI	YGMALNATSYPSV-----VQAMSIDGGIRAATSQEINELTYTTLSANS	121
MDLA_PENCA	-----YeadyTAQVGDKL	60
LIP_RHIDL	YCRSVVPGNKWDCVQCQKWVPDGKIITFT-SLLSDTNGYVLRSDKQKTI	199
LIP_RHIMI	YCRTVIPGATWDCIHCDAT-EDLKIITWS-TLIYDTNAMVARGDSEKTI	169
MDLA_PENCA	SCSKG- - - - -NCPEVEA - -TGATVSYDFSDDITDTAGYIAVDHTNSAV	102

Page 29, line 4, please rewrite the paragraph thereat as follows:

**Peptide 1**

**VHTGFWK (SEQ ID NO: 2)**

**Peptide 2**

**AWESAADELTSK (SEQ ID NO: 19)**

LIP_RHIDL	YLVFRGTNSFRSAITDIVFNFSYKPVKGAKVHAGFLSSYEQVVNDYFPV	249
LIP_RHIMI	YIVFRGSSSIRNW IADLTFVPVSYPVSGTKVHKGLDSYGEVQNELVAT	219
MDLA_PENCA	VLAFRGSYSVRNWWADATFVHTNPGLCDGCLAELGFWSSWKLVRDDIIE	152
	. . . . . * * . . . . * . . . . * . . . . * . . . . *	

**Peptide 2 IK**

LIP_RHIDL	VQEQLTAHPTYKVIVTGHSLGGAQALLAGMDLYQREPRISPKNLSIFTVG	299
LIP_RHIMI	VLDQFKQYPSYKVAVTGHSLGGATALLCALDLYQREEGLSSSNLFLYTQG	269
MDLA_PENCA	LKEVVAQNPNYELVVVGHSLGAAVATLAATDL -- RGKGYPsakLYAYA--	198
	. . . . . * . . . . * . . . . * . . . . * . . . . *	

LIP_RHIDL	GPRVGNPTFAYYVESTGPFQRTVHKRDIVPHVPPQSFGFLHPGESWIK	349
LIP_RHIMI	QPRVGDPAFANYVVSTGIPYRRTVNERDIVPHLPAAFGFLHAGEEYWIT	319
MDLA-PENCA	SPRVGNAALAKYITAQGNF-RFHTNDPVPKLPLLSMGYVHVSPEYWIT	247
	*** . . . . * . . . . * . . . . * . . . . * . . . . *	

LIP_RHIDL	SGTSN - V - - - - QICTSEIETKDCSNSIVPFTSILD - HLSYF - DINEGSC	391
LIP_RHIMI	DNSPETV - - - - - QVCTSDLETSDCSNSIVPFTSVLD - HLSYF - GINTGLC	362
MDLA_PENCA	SPNNATVSTSDIKVIDGDVSFDGNTGTGLPLLTDFAHIWYFVQDAGKG	297

LIP_RHIDL	----- L	392
LIP_RHIMI	----- T	363
MDLA_PENCA	PGLPFKRV	305

Page 30, line 37, please rewrite the paragraph thereat as follows:

Degenerated primers for PCR amplification of a fragment of the lipase gene were designed based on the amino acid sequence of the isolated peptides. The following three PCR primers were synthesized:

C035: TTC CAR YTN TTY GCN CAR TGG (SEQ ID NO: 5)

18 mer 256 mixture, based on the N-terminal sequence QLFAQW. (SEQ ID NO: 21)

C037: GCV GCH SWY TCC CAV GC (SEQ ID NO: 6)

17 mer 216 mixture, based on internal peptide 2 sequence AWESAA (reversed). (SEQ ID NO: 22)

Page 33, line 7, please rewrite the paragraph thereat as follows:

Table 5.1. (SEQ ID NO: 13)PCR-generated putative *lipA* sequence

(The four amino acid fragments of table 5.1 are contained in SEQ ID NOS: 14-17)

10	20	30	40	50	60
taccgggntccattCAGTTGTTTCGCGCAATGGTCTGCCGCAGCTTATTGCTCGAATA					

Q	L	F	A	Q	W	S	A	A	A	Y	C	S	N
70	80	90	100	110	120								

ATATCGACTCGAAAGAVTCCAACCTTGACATGCACGGCCAACGCCTGTCCATCAGTCGAGG  
N I D S K X S N L T C T A N A C P S V E

130	140	150	160	170	180														
AGGCCAGTACCACGATGCTGCTGCTGGTGGAGTTCGACCTGTATGTCACTCAGATCGCAGACATAG																			
E	A	S	T	T	M	L	L	E	F	D	L	Y	V	T	Q	I	A	D	I
190	200	210	220	230	240														
AGCACAGCTAATTGAACAGGACGAACGACTTTTGGAGGCACAGCCGGTTTCCTGGCCGCG																			
E	H	S	-	L	N	R	T	N	D	F	W	R	H	S	R	F	P	G	R
250	260	270	280	290	300														
G	Q	H	Q	Q	A	A	R	G	R	L	P	G	K	Q	H	D	-	E	L

310 320 330

ATTGCTAATCYTGACTTCATCCTGGRAGATAACG

DC - X - LHPXR - (SEQ ID NO: 13)

Page 37, line 10, please rewrite the paragraph thereat as follows:

The gene was sequenced using cycle sequencing and conventional sequencing technology. The complete sequence (SEQ ID NO: 18) is shown below in Table 6.1. The sequence has been determined for both strands for the complete coding region and about 100bp upstream and downstream of the coding region. The sequences downstream to the coding region have only been determined on one strand and contain a few uncertainties. In the sequence as shown below, the intron sequences are indicated as lowercase letters and the N-terminal and the two internal peptides (peptide 1 and peptide 2) are underlined:

Page 37, line 22, please rewrite the paragraph thereat as follows:

Table 6.1. (SEQ ID NO: 18) The DNA sequence for the lipA gene and flanking sequences

```

1      CCNDTTAATCCCCACCGGGTTCCCGCTCCCGGATGGAGATGGGGCCAAACTGGCAAC
61     CCCCAGTTGCGCAACGGAACAACCGCCGACCCGGAACAAAGGATGCGGATGAGGAGATAC
121    GGTGCCTGATTGCATGGCTGGCTTCATCTGCTATCGTGACAGTGCTCTTTGGGTGAATAT
181    TGTTGTCTGACTTACCCCGCTTCTTGCTTTTTCCCCCTGAGGCCCTGATGGGGAATCGC
241    GGTGGGTAATATGATATGGGTATAAAAGGGAGATCGGAGGTGCAGTTGGATTGAGGCAGT
301    GTGTGTGTGTCATTGCAGAAGCCCGTTGGTCGCAAGGTTTTGGTCGCCTCGATTGTTTG
361    TATACCGCAAGATGTTCTCTGGACGGTTTGGAGTGCTTTTGACAGCGCTTGCTGCGCTGG
        M F S G R F G V L L T A L A A L
421    GTGCTGCCGCGCCGGCACCCTTGCTGTGCGGAgtaggtgtgcccgatgtgagatggttg
        G A A A P A P L A V R
481    gatagcactgatgaagggtgaatagGTGTCTCGACTTCCACGTTGGATGAGTTGCAATTG
        S V S T S T L D E L Q L
541    TTCGCGCAATGGTCTGCCGACGCTTATTGCTCGAATAATATCGACTCGAAAGACTCCAAC
        F A Q W S A A A Y C S N N I D S K D S N
601    TTGACATGCACGGCCAACGCCTGTCCATCAGTCGAGGAGGCCAGTACCACGATGCTGCTG
        GAGTTCGACCTgtatgtcactcagatcgacacatagagcacagctaatttgaacagGAC
        E F D L
721    GAACGACTTTGGAGGCACAGCCGGTTTCCTGGCCGCGGACAACACCAACAAGCGGCTCGT
        N D F G G T A G F L A A D N T N K R L V
781    GGTGCTTCCGGGGAAGCAGCAGATTGAGAAGTGGATTGCTAATCTTGACTTCATCCT
        V A F R G S S T I E N W I A N L D F I L
841    GGAAGATAACGACGACCTCTGCACCGGCTGCAAGGTCCATACTGGTTTCTGGAAGGCATG
        E D N D D L C T G C K V H T G F W K A W
901    GGAGTCCGCTGCCGACGAAGTACGAGCAAGATCAAGTCTGCGATGAGCACGTATTCCGG
        E S A A D E L T S K I K S A M S T Y S G
961    CTATACCCTATACTTACCGGGCACAGTTTGGGCGGCGCATTGGCTACGCTGGGAGCGAC
        Y T L Y F T G H S L G G A L A T L G A T
1021   AGTTCTGCGAAATGACGGATATAGCGTTGAGCTGGTGAGTCCTTCACAAAGGTGATGGAG

```

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V L R N D G Y S V E L
1081 CGACAATCGGGAACAGACAGTCAATAGTACACCTATGGATGTCCTCGAATCGGAAACTAT
      Y T Y G C P R I G N Y
1141 GCGCTGGCTGAGCATATCACCAGTCAGGGATCTGGGGCCAACTTCCGTGTTACACACTTG
      A L A E H I T S Q G S G A N F R V T H L
1201 AACGACATCGTCCCCCGGTGCCACCCATGGACTTTGGATTTCAGTCAGCCAAGTCCGGAA
      N D I V P R V P P M D F G F S Q P S P E
1261 TACTGGATCACCAGTGGCAATGGAGCCAGTGTACGGCGTCGGATATCGAAGTCATCGAG
      Y W I T S G N G A S V T A S D I E V I E
1321 GGAATCAATTCAACGGCGGGAAATGCAGGCGAAGCAACGGTGAGCGTTGTGGCTCACTTG
      G I N S T A G N A G E A T V S V V A H L
1381 TGGTACTTTTTTGCATTTCGAGTGCCTGCTATAACTAGACCGACTGTCAGATTAGTGG
      W Y F F A I S E C L L -
1441 ACGGGAGAAGTGTACATAAGTAATTAGTATATAATCAGAGCAACCCAGTGGTGGTGTATGG
1501 TGGTGAAAGAAGAAACACATTGAGTTCCCATACGKAGCAGWTAAAGCACTKKGGAGGC
1561 GCTGGTTCCTCCACTTGGCAGTTGGCGGCCATCAATCATCTTCTCCTTACTTTTCGT
1621 CCACCACAACCTCCCATCTGCCAGCTGTGCGATCCCCGGGTGCAACAACATATCGCCTCC
1681 GGGGCCTCCGTGGTTCTCCTATATTATCCATCCGACGGCCGACGTTTCACCCCTCAACCT
1741 GCGCCGCCGCAAAATCTCCCCGAGTCGGTCAACTCCCTCGAACCGCCGCCGCATCGACC
1801 TCACGACCCCGACCGTCTGYGATYGTCCAACCG

```

Page 39, line 1, please rewrite the table thereat as follows:

Table 6.2 Alignment of the lipase 3 sequence with known fungal lipases

LIPASE 3	MFSG ----- RFGVLL -----TALAA	-15
MDLA_PENCA	MRLS ----- FETAL ----- SAVAS	-14
LIP_RHIDL	MVSFISISQGVSLCLLVSSMMLGSSAVPVSGKSGSSNTAVSADNAALPP	-50
LIP_RHIMI	MVLKQRANYLGFLIVFFTAFLV -- EAVPIKRQSNSTVDS- ----- LPP	-40
LIPASE 3	L -----	-16
MDLA_PENCA	L -----	-15
LIP_RHIDL	LISSRCAPPSNKGSKSDLQAEPYNMQKNTEWYESHGGNLTSGIKRDDNLV	-100
LIP_RHIMI	LIPSRTSAPSSSPSTTDPEAPAM ----- SRNGPLPS ---- DVETK	-76
LIPASE 3	-----GAAAPAPLA-----VRSVSTSTLDELQLFAQWSAAA	-47
MDLA_PENCA	-----GYALPGKLQ-----SRDVSTSELDQFEFVWQYAAAS	-46
LIP_RHIDL	GGMTLDLPDAPPISLSSSTNSASDGGKVVAATTAQIQEFTKYAGIAATA	-150
LIP_RHIMI	YGMALNATSYPDVS-----VQAMSIDGGIRAATSQEINELTYTTLSANS	-121
LIPASE 3	YCSNNIDSK-DSNLTCTANACPSVEEASTTMLLEFDLTNDFGGTAGFLAA	-96
MDLA_PENCA	YYEADYTAQVGDKLSCSKGNCPEVEATGATVSYDFS-DSTITDTAGYIAV	-95
LIP_RHIDL	YCRSVVP---GNKWDCVQ---CQKWVPDGKIIT---TFTSLLSDTNGYVLR	-192
LIP_RHIMI	YCRTVIP---GATWDCIH---CDA-TEDLKIHK---TWSTLIYDTNAMVAR	-162
LIPASE 3	DNTNKRLVVAFRGSSTIENWIANLDFILEDNDDLCTGCKVHTGFWKAWES	-146
MDLA_PENCA	DHTNSAVVLAFRGSYSVRNWVADATFV-HTNPGLCDGCLAELGFWSSWKL	-144

LIP_RHIDL	SDKQKTIYLVFRGTNSFRSAITDIVNFSDYKPV-KGAKVHAGFLSSYEQ	-241
LIP_RHIMI	GDSEKTIYIVFRGSSSIRNWIADLTFVPVSYPPV-SGTKVHKGF LDSYGE	-211
LIPASE 3	AADELTSKIKSAMSTYSGYTLYFTGHSLGGALATLGATVL—RNDGY-SV	-193
MDLA_PENCA	VRDDIIKELKEVVAQNPNYELVVVGHSLGAAVATLAATDL—RGKGYPSA	-192
LIP_RHIDL	VVNDYFPVVQEQLTAHPTYKVIVTGHSLGGAQALLAGMDLYQREPRLSPK	-291
LIP_RHIMI	VQNELVATVLDQFKQYPSYKVAVTGHSLGGATALLCALDLYQREEGLSSS	-261
LIPASE 3	ELYTY—GCPRIGNYALAEHITSQGSGANFRVTHLNDIVPRVPPMDFGFS	-241
MDLA_PENCA	KLYAY - - ASPRVGNAALAKYITAQGN - - NFRFHTNDPVPKPLLLSMGYV	-238
LIP_RHIDL	NLSIFTVGGPRVGNPTFAYYVESTGIPFQ-RTVHKRDIVPHVPPQSFGFL	-340
LIP_RHIMI	NFLYTQGGQPRVGDPAFANYVVSTGIPYR-RTVNERDIVPHLPPAAFGL	-310
LIPASE 3	QPSPEYWITSGNGASVTASDIEVIEGINSTAGNAGEATVSVV---AHLWY	-288
MDLA_PENCA	HVSPEYWITSPNNATVSTSDIKVIDGDVSFDGNTGTGLPLLTDFEAHIWY	-288
LIP_RHIDL	HPGVESWIKSGTSN-VQICTSEIE-----TKDCSNSIVPETSILDHLSY	-383
LIP_RHIMI	HAGEEYWITDNSPETVQVCTSDLE-----TSDCSNSIVPFTSVLDHLSY	-354
LIPASE 3	FFAISECL- - - - -L	-297 (SEQ ID NO: 9)
MDLA_PENCA	FVQVDAGKGPGLPFKRV	-305 (SEQ ID NO: 12)
LIP_RHIDL	F - DINEGSC- - - - -L	-392 (SEQ ID NO: 10)
LIP_RHIMI	F - GINTGLC- - - - -T	-363 (SEQ ID NO: 11)

\* ...

Page 40, line 31, please rewrite the table thereat as follows:

Table 6.3 Alignment of coding sequence of the *lipA* gene and gene coding for mono-diacyl lipase from *Penicillium camemberti*

LIPASE 3	MFSGRFGVLLTALAALGAAAPLA VRSVSTLDELQLFAQWSAAAYCS	-50
MDLA_PENCA	MRLSFFTAL - SAVASLGYALPGKLQSRDVTSELDQFEFWVQYAAASYE	-49
LIPASE 3	NN I DSK - DSNLTCTANACPSVEEASTTMLLEFDLTNDFGGTAGFLAADNT	-99
MDLA_PENCA	ADYTAQVGDKLSCSKGNCPEVEATGATVSYDFS - DSTITDTAGY IAVDHT	-98
LIPASE 3	NKRLVVAFRGSSTIENW I ANLDFILEDNDDLCTGCKVHTGFWKAWESAAD	-149
MDLA_PENCA	NSAVVLAFRGSYSVRNWVADATFV-HTNPGLCDGCLAELGFWSSWKLVRD	-147

LIPASE 3	ELTSKIKSAMSTYSGYTLYFTGHSLGGALATLGATVLRNDGY-SVELYTY	-198
MDLA_PENCA	DIIKELKEVVAQNPNYELVVVGHSLGAAVATLAATDLRGKGYPYSAKLYAY	-197
LIPASE 3	GCPR IGNYALAEHITSQGSGANFRVTHLNDIVPRVPPMDFGFSQPSPEYW	-248
MDLA_PENCA	ASPRVGNAALAKYITAQGN- - NFRFHTNDPVPKLPLLSMGYVHVSPEYW	-245
LIPASE 3	ITSGNGASVTASDIEVIEGINSTAGNAGEATVSVV - - - AHLWYFFAISEC	-295
MDLA_PENCA	ITSPNNATVSTSDIKVIDGDVSFDGNTGTGLPLLTDTFEAWYFVQVDAG	-295
LIPASE 3	L-----L -297 (SEQ ID NO: 9)	
MDLA_PENCA	KGPGLPFKRV -305 (SEQ ID NO: 12)	

Identity: 126 amino acids (42.42%)

Page 41, line 30, please rewrite the paragraph thereat as follows:

Table 6.4: Amino acid sequence of the precursor of lipase 3 (SEQ ID NO: 9)

	5	10	15	20	25	30																								
1	M	F	S	G	R	F	G	V	L	L	T	A	L	A	A	L	G	A	A	P	A	P	L	A	V	R	S	V	S	
31	T	S	T	L	D	E	L	Q	L	F	A	Q	W	S	A	A	A	Y	C	S	N	N	I	D	S	K	D	S	N	L
61	T	C	T	A	N	A	C	P	S	V	E	E	A	S	T	T	M	L	L	E	F	D	L	T	N	D	F	G	G	T
91	A	G	F	L	A	A	D	N	T	N	K	R	L	V	V	A	F	R	G	S	S	T	I	E	N	W	I	A	N	L
121	D	F	I	E	D	N	D	D	L	C	T	G	C	K	V	H	T	G	F	W	K	A	W	E	S	A	A	D	E	
151	L	T	S	K	I	K	S	A	M	S	T	Y	S	G	Y	T	L	Y	F	T	G	H	S	L	G	G	A	L	A	T
181	L	G	A	T	V	L	R	N	D	G	Y	S	V	E	L	Y	T	Y	G	C	P	R	I	G	N	Y	A	L	A	E
211	H	I	T	S	Q	G	S	G	A	N	F	R	V	T	H	L	N	D	I	V	P	R	V	P	P	M	D	F	G	F
241	S	Q	P	S	P	E	Y	W	I	T	S	G	N	G	A	S	V	T	A	S	D	I	E	V	I	E	G	I	N	S
271	T	A	G	N	A	G	E	A	T	V	S	V	V	A	H	L	W	Y	F	F	A	I	S	E	C	L	L			

Number of residues: 297

Please replace the previously filed sequence listing with the enclosed papers titled --  
sequence listing.--